

FIG.1A

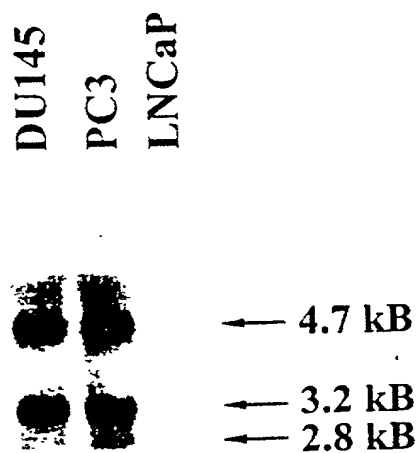


FIG.1B

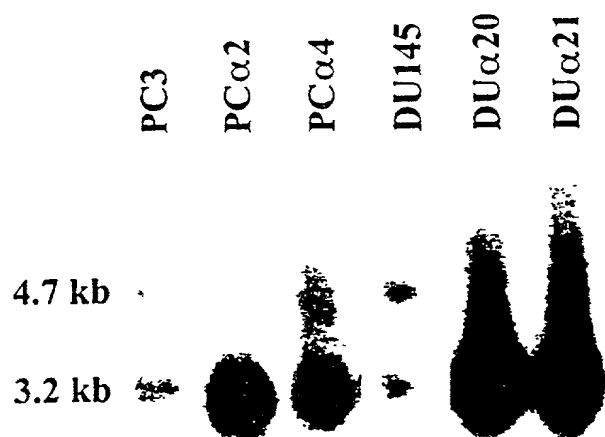


FIG.2



DU145



DU $\alpha$ 20



DU $\alpha$ 21

FIG.3A



PC3



PC $\alpha$ 2



PC $\alpha$ 4

FIG.3B

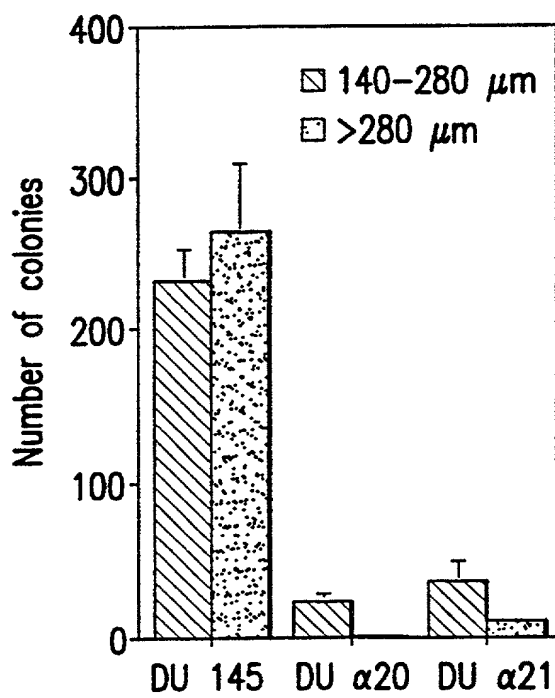


FIG.3A-1

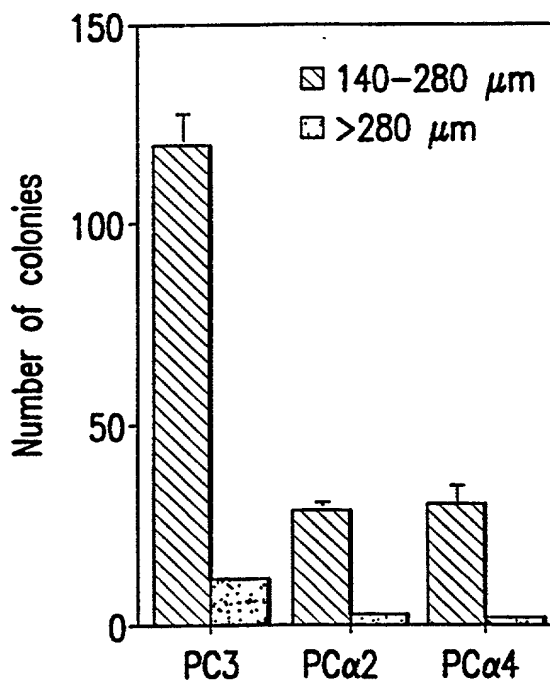


FIG.3B-1

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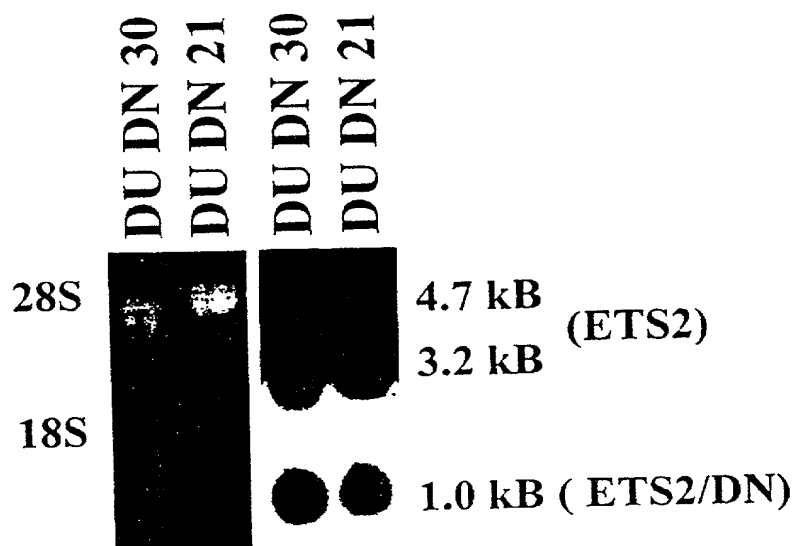


FIG.4A

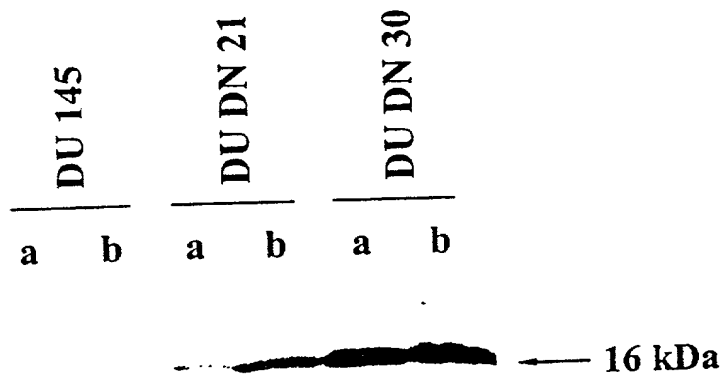


FIG.4B

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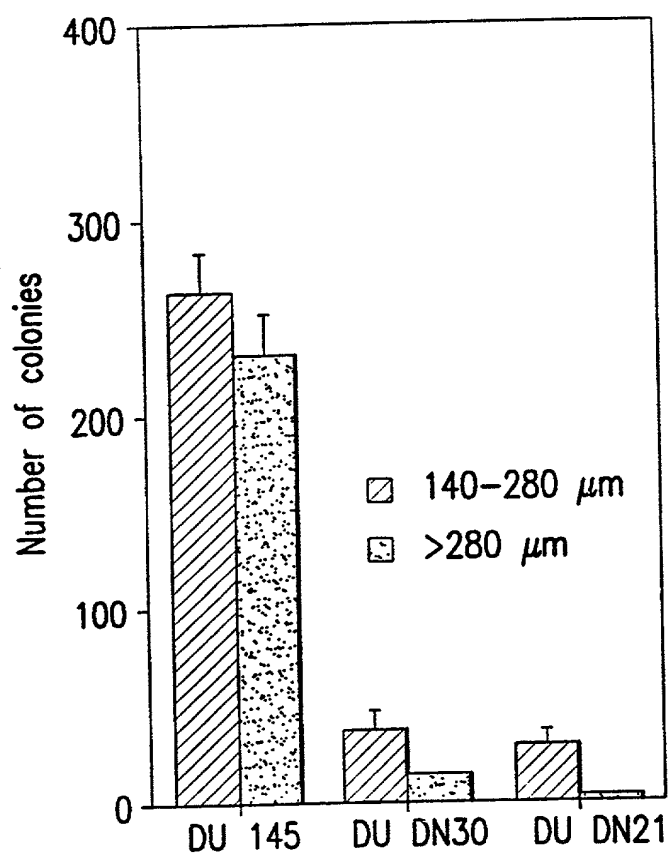


FIG.5

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CCGTTTCCTC CCCTCCCCTC CACTCGGCGG TCCCTCCTTC CTCCTCCCTC CTCCTCCTC 60  
 CTCCCGCTCC TGAAGAGCGC GCCGCGTGGG GGACGGCCCC GTTACTTCCT CCAGAGACTG 120  
 ACGAGTGGCG TGTCGCTCCA GCTCAGAGCT CCCGAGCCG CCCGGCCAGC GTCCGGCCTC 180  
 CCTGATCGTC TCTGGCCGCG GCCCTGCCCC TCGCCCGGCG CGCACCGAGC AGCCGCGGGC 240  
 GCCGAGCAGC CACCGTCCCG ACCAAGCGCC GGCCCTGCCC GCAGCGGCAG GATGAATGAT 300  
 TTCGGAATCA AGAATATGGA CCAGGTAGCC CCTGTGGCTA ACAGTTACAG AGGGACACTC 360  
 AAGCGCCAGC CAGCCTTTGA CACCTTTGAT GGGTCCCTGT TTGCTGTTTT TCCTTCTCTA 420  
 AATGAAGAGC AAACACTGCA AGAAGTCCA ACAGGCTTGG ATTCCATTTC TCATGACTCC 480  
 GCCAACTGTG AATTGCCCTT GTTAACCCCG TGCAGCAAGG CTGTGATGAG TCAAGCCTTA 540  
 AAAGCTACCT TCAGTGGCTT CAAAAAGGAA CAGCGGCGCC TGGGCATTCC AAAGAACCCC 600  
 TGGCTGTGGA GTGAGCAACA GGTATGCCAG TGGCTTCTCT GGGCCACCAA TGAGTTCAGT 660  
 CTGGTGAACG TGAATCTGCA GAGGTTCCGC ATGAATGGCC AGATGCTGTG TAACCTTGGC 720  
 AAGGAACGCT TTCTGGAGCT GGCACCTGAC TTTGTGGTG ACATTCTCTG GGAACATCTG 780  
 GAGCAAATGA TCAAAGAAAA CCAAGAAAAG ACAGAAGATC AATATGAAGA AAATTCACAC 840  
 CTCACCTCCG TTCCTCATTG GATTAACAGC AATACATTAG GTTTTGGCAC AGAGCAGGCG 900  
 CCCTATGGAA TGCAGACACA GAATTACCCC AAAGGCGGCC TCCTGGACAG CATGTGTCCG 960  
 GCCTCCACAC CCAGCGTACT CAGCTCTGAG CAGGAGTTTC AGATGTTCCC CAAGTCTCGG 1020  
 CTCAGCTCCG TCAGCGTCAC CTACTGCTCT GTGAGTCAGG ACTTCCCAGG CAGCAACTTG 1080  
 AATTTGCTCA CCAACAATTC TGGGACTCCC AAAGACCACG ACTCCCTGA GAACGGTGCG 1140  
 GACAGCTTCG AGAGCTCAGA CTCCCTCCTC CAGTCTGGA ACAGCCAGTC GTCCTTGCTG 1200  
 GATGTGCAAC GGGTTCCTTC CTTGAGAGC TTGGAAGATG ACTGCAGCCA GTCTCTCTGC 1260  
 CTCAATAAGC CAACCATGTC TTTCAAGGAT TACATCCAAG AGAGGAGTGA CCCAGTGGAG 1320  
 CAAGGCAAC CAGTTATACC TGCAGCTGTG CTGGCCGGCT TCACAGGAAG TGGACCTATT 1380  
 CAGCTGTGGC AGTTTCTCCT GGAGCTGCTA TCAGACAAAT CCTGCCAGTC ATTCATCAGC 1440  
 TGGACTGGAG ACGGATGGCA GTTTAAGCTC GCCGACCCCG ATGAGGTGGC CCGCCGTTGG 1500  
 GGAAAGAGGA AAAATAAGCC CAAGATGAAC TACGAGAAGC TGAGCCGGGG CTTACGCTAC 1560  
 TATTACGACA AGAACATCAT CCACAAGACG TCGGGGAAGC GCTACGTGTA CCGCTTCGTG 1620  
 TGCGACCTCC AGAACTTGCT GGGGTTACG CCCGAGGAAC TGCACGCCAT CCTGGGCGTC 1680  
 CAGCCCGACA CGGAGGACTG AGGTGCGCGG GACCACCCTG AGCCGCCCC AGGCTCGTGG 1740  
 ACTGAGTGGG AAGCCCATCC TGACCAGCTG CCTCCGAGGA CCCAGGAAAG GCAGGATTGA 1800  
 AAATGTCCAG GAAAGTGGCC AAGAAGCAGT GGCCTTATTG CATCCCAAAC CACGCCTCTT 1860  
 GACCAGGCTG CCTCCCTTGT GGCAGCAACG GCACAGCTAA TTCTACTCAC AGTGCTTTTA 1920  
 AGTGAAAATG GTCGAGAAAG AGGCACCGGG AAGCCGTCCT GCGCCTGGC AGTCCGTGGG 1980  
 ACGGGATGGT TCTGGCTGTT TGAGATTCTC AAAGGAGCGA GCATGTCGTG GACACACACA 2040  
 GACTATTTTT AGATTTTCTT TTGCCTTTTG CAACCAGGAA CAGCAAATGC AAAAATCTT 2100  
 TGAGAGGGTA GGAGGGTGGG AAGGAAACAA CCATGTCATT TCAGAAGTTA GTTTGTATAT 2160  
 ATTATAATAA TCTTATAATT GTTCTCAGAA TCCCTTAACA GTTGTATTTA ACAGAAATTG 2220  
 TATATTGTAA TTTAAATAA TTATATAACT GTATTGAAA TAAGAATTC 2269

FIG. 6

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Met Asn Asp Phe Gly Ile Lys Asn Met Asp Gln Val Ala Pro Val Ala  
 1 5 10 15  
 Asn Ser Tyr Arg Gly Thr Leu Lys Arg Gln Pro Ala Phe Asp Thr Phe  
 20 25 30  
 Asp Gly Ser Leu Phe Ala Val Phe Pro Ser Leu Asn Glu Glu Gln Thr  
 35 40 45  
 Leu Gln Glu Val Pro Thr Gly Leu Asp Ser Ile Ser His Asp Ser Ala  
 50 55 60  
 Asn Cys Glu Leu Pro Leu Leu Thr Pro Cys Ser Lys Ala Val Met Ser  
 65 70 75 80  
 Gln Ala Leu Lys Ala Thr Phe Ser Gly Phe Lys Lys Glu Gln Arg Arg  
 85 90 95  
 Leu Gly Ile Pro Lys Asn Pro Trp Leu Trp Ser Glu Gln Gln Val Cys  
 100 105 110  
 Gln Trp Leu Leu Trp Ala Thr Asn Glu Phe Ser Leu Val Asn Val Asn  
 115 120 125  
 Leu Gln Arg Phe Gly Met Asn Gly Gln Met Leu Cys Asn Leu Gly Lys  
 130 135 140  
 Glu Arg Phe Leu Glu Leu Ala Pro Asp Phe Val Gly Asp Ile Leu Trp  
 145 150 155 160  
 Glu His Leu Glu Gln Met Ile Lys Glu Asn Gln Glu Lys Thr Glu Asp  
 165 170 175  
 Gln Tyr Glu Glu Asn Ser His Leu Thr Ser Val Pro His Trp Ile Asn  
 180 185 190  
 Ser Asn Thr Leu Gly Phe Gly Thr Glu Gln Ala Pro Tyr Gly Met Gln  
 195 200 205  
 Thr Gln Asn Tyr Pro Lys Gly Gly Leu Leu Asp Ser Met Cys Pro Ala  
 210 215 220  
 Ser Thr Pro Ser Val Leu Ser Ser Glu Gln Glu Phe Gln Met Phe Pro  
 225 230 235 240  
 Lys Ser Arg Leu Ser Ser Val Ser Val Thr Tyr Cys Ser Val Ser Gln  
 245 250 255  
 Asp Phe Pro Gly Ser Asn Leu Asn Leu Leu Thr Asn Asn Ser Gly Thr  
 260 265 270  
 Pro Lys Asp His Asp Ser Pro Glu Asn Gly Ala Asp Ser Phe Glu Ser  
 275 280 285  
 Ser Asp Ser Leu Leu Gln Ser Trp Asn Ser Gln Ser Ser Leu Leu Asp  
 290 295 300  
 Val Gln Arg Val Pro Ser Phe Glu Ser Phe Glu Asp Asp Cys Ser Gln  
 305 310 315 320  
 Ser Leu Cys Leu Asn Lys Pro Thr Met Ser Phe Lys Asp Tyr Ile Gln  
 325 330 335



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Glu Arg Ser Asp Pro Val Glu Gln Gly Lys Pro Val Ile Pro Ala Ala  
                   340                                  345                                  350  
 Val Leu Ala Gly Phe Thr Gly Ser Gly Pro Ile Gln Leu Trp Gln Phe  
                   355                                  360                                  365  
 Leu Leu Glu Leu Leu Ser Asp Lys Ser Cys Gln Ser Phe Ile Ser Trp  
                   370                                  375                                  380  
 Thr Gly Asp Gly Trp Glu Phe Lys Lau Ala Asp Pro Asp Glu Val Ala  
 385                                  390                                  395                                  400  
 Arg Arg Trp Gly Lys Arg Lys Asn Lys Pro Lys Met Asn Tyr Glu Lys  
                                   405                                  410                                  415  
 Leu Ser Arg Gly Leu Arg Tyr Tyr Tyr Asp Lys Asn Ile Ile His Lys  
                                   420                                  425                                  430  
 Thr Ser Gly Lys Arg Tyr Val Tyr Arg Phe Val Cys Asp Leu Gln Asn  
                   435                                  440                                  445  
 Leu Leu Gly Phe Thr Pro Glu Glu Leu His Ala Ile Leu Gly Val Gln  
                   450                                  455                                  460  
 Pro Asp Thr Glu Asp  
 465

FIG.7B

ETS1	HUMAN	SG-P IQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKL SRGLRYYYDKNIIRKTA-GKRYVYRFV-
ETS1	MOUSE	SG-P IQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKL SRGLRYYYDKNIIRKTA-GKRYVYRFV-
ETSB	CHICK	SG-P IQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKL SRGLRYYYDKNIIRKTA-GKRYVYRFV-
ETSA	XENLA	SG-P IQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKL SRGLRYYYDKNIIRKTA-GKRYVYRFV-
vETS	E26	SG-P IQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKL SRGLRYYYDKNIIRKTA-GKRYVYRFV-
ETS2	XENLA	SG-P IQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKL SRGLRYYYDKNIIRKTA-GKRYVYRFV-
ETS2	HUMAN	SG-P IQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKL SRGLRYYYDKNIIRKTA-GKRYVYRFV-
ETS2	MOUSE	SG-P IQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKL SRGLRYYYDKNIIRKTA-GKRYVYRFV-
ETS2	CHICK	SG-P IQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWGKRK-WEPKMNYEKL SRGLRYYYDKNIIRKTA-GKRYVYRFV-
ETS2	SEAU R	SG-P IQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWG IRK-WEPKMNYEKL SRGLRYYYDKNIIRKTA-GKRYVYRFV-
ETS2	DROME	SG-P IQLWQFLLELLTDKS-COSFISWTG-DGWEFKLS--DPDEVARRWG IRK-WEPKMNYEKL SRGLRYYYDKNIIRKTA-GKRYVYRFV-
FLI1	MOUSE	SG-Q IQLWQFLLELLSDS-NASCI TWEG-TNGEFKMT--DPDEVARRWG ERK-SKPNNMYD KL SRALRYYYDKNIMTKVH-GKRYAYKF D-
ERG	HUMAN	SG-Q IQLWQFLLELLSDS-NASCI TWEG-TNGEFKMT--DPDEVARRWG ERK-SKPNNMYD KL SRALRYYYDKNIMTKVH-GKRYAYKF D-
ETS3	DROME	GSGQIQ WQPLLELLSDSN-NASCITWEGTNG EFKLT--DPDEVARRWG ERK-SKPNNMYD KL SRALRYYYDKNIMTEVH-GKRYAYKF D-
ETS6	DROME	SCGQIQ L WQPLLELLADSS-NANA ISWEG-QSGEFR LI--DPDEVARRWG ERK-AKPNNMYD KL SRALRYYYDGDMICVKQ-GKGF VYKFV-
GABP	RAT	NC-Q IQLWQFLLELLTDKD-ARDCISWVG-DEGEFKLN--QP ELVAQKWQRK-NKPTMNPYKL SRALRYYYDGDMISKVS-GQKF VYKFV-
DELG	DROME	NC-QVQLWQFLLEILLTDCE-HTDV IEWVG-TEGEFKLT--DPDRVARLWGEKK-NKPTMNPYKL SRALRYYYDGDMISKVS-GQKF VYKFV-
PEA3	MOUSE	RGA-LQLWQFLVALLDPT-NARFLAWTG-RQMEFKLI--EPEEVARLWGIQ-NRPAMNMDKL SRSLRYYEKG IMQKVA-GERVYKFV-
ELK	HUMAN	MDPSTLVWQFLLOLLREQG-NGHI ISNTSRDGGCFKL V--DAEEVARLWGLRK-NKTNMNTDKL SRALRYYYQKNII RKVS-GQKF VYKFV-
SAP1	HUMAN	MDSAITLVWQFLLOLLQKPQ-NKHMCWTSNDG-QFKLL--QAEEVARLWGIQ-NKPNNMYD KL SRALRYYYVYKNII KKV N-GQKVYKFVS-
ELKX	MOUSE	LWQFLLELLLDQN-HDHL ICNTSNDG-QFKLL--KAEEVARLWGLRK-NE TNMNYD KL SRALR
ELF1	HUMAN	KGN TIYLWEFLALLQDKATCPKYIKWTOREKGI FKL V--DSKAVSRL WGKHK-NKEDMN YE TMGRALRYYYQRG ILAKVE-GQRL VIQFK
E74A	DROME	EGSTTYLWEFLALLQDREYCPRFI KWTNREKGVFKL V--DSKAVSRL WGMHK-NKEDMN YE TMGRALRYYYQRG ILAKVD-GQRL VIH FV
ETS4	DROME	GGSHIHLWQFLIKELLASPVQNGTAIRWI DRSKGIPKIE--DSVRVAKLWGRRK-NRPAMNMDKL LRSIRQYVYKKG IMKKSERSQRL VYOF C
PUI	MOUSE	SKKKIRLYQFLDLLRSGDM-KDSIWVVDKDKGTQFSSKHKEALAHRWGIQKGNRKKN TYQKMARAL RNYGKTGEVKKVK--KKLTYQF-S
PUI	HUMAN	SKKKIRLYQFLDLLRSGDM-KDSIWVVDKDKGTQFSSKHKEALAHRWGIQKGNRKKN TYQKMARAL RNYGKTGEVKKVK--KKLTYQF-S

**FIG. 8A**

**FIG. 8B**

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ETS2 IN 289

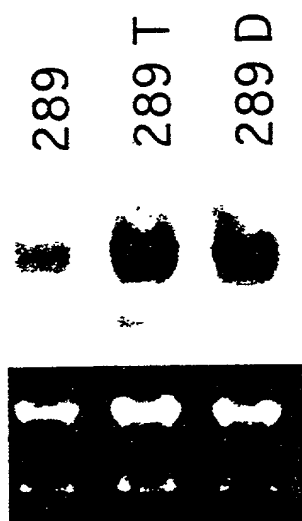


FIG.9A

ETS1 IN 289

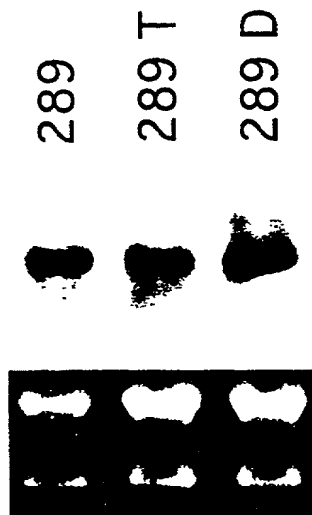


FIG.9B

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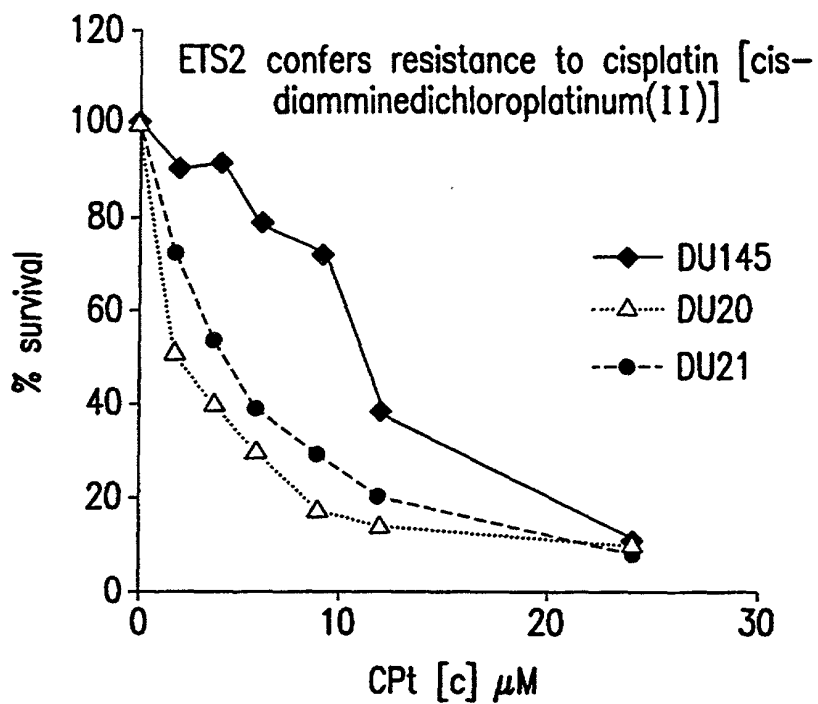


FIG.10